

A NOVEL METHOD TO REPRESENT ECG SIGNALS VIA PREDEFINED PERSONALIZED SIGNATURE AND ENVELOPE FUNCTIONS

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Abstract-In this paper, a new method to model ECG signals by means of "Predefined Personalized Signature and Envelope Functions" is presented. ECG signals are somewhat unique to a person. Moreover, it presents quasi-stationary behavior. Therefore in this work, on a frame basis, personal ECG signals $X_i(t)$ is modeled by the form of $X_i(t) \approx C_i \phi_i(t) \alpha_i(t)$. In this model, $\phi_i(t)$ is defined as the *Personalized Signature Function (PSF)*; $\alpha_i(t)$ is referred to as *Personalized Envelope Function (PEF)* and C_i is called the *Frame-Scaling Coefficient (FSC)*. It has been demonstrated that for each person, the sets $\Phi=\{\phi_k(t)\}$ and $A=\{\alpha_k(t)\}$ constitute a "Predefined Personalized Functional Bases or Banks (PPFB)" to describe any measured ECG signal. Almost optimum forms of (PPFB), namely $\{\alpha_k(t)\}$, $\{\phi_k(t)\}$ pairs are generated in the Least Mean Square (LMS) sense. Thus, ECG signal for each frame is described in terms of the two indices "R" and "K" of PPFB and the frame-scaling coefficient C_i . It has been shown that the new method of modeling provides significant data compression. Furthermore, once PPFB are stored on each communication node, transmission of ECG signals reduces to the transmission of indexes "R" and "K" of $[\alpha_k(t), \phi_k(t)]$ pairs and the coefficients C_i , which also result in considerable saving in the transmission band.

Keywords - Models, Compression, Transmission of ECG Signals

I. INTRODUCTION

Biomedical signals are used widely in diagnosis and therapy of many diseases. The processing, storing and transfer of biological signals is gaining ever more importance in today's information era. However, since such signals comprise huge amounts of data, the storage, transfer and reconstruction of biological signals create certain limitations. One way to overcome this problem is the compression of the signals, provided that the information covered by the signal is not lost. Moreover, such signals have to be repeatedly received and evaluated during the course of the illness in order to verify the diagnosis, determine the treatment method(s) and allow follow up of the therapy to avoid abnormal patterns and complications. Therefore, compression of signals with acceptable loss is inevitable.

Diagnosis, compression and speedy transmission of the ECG signals may be achieved by means of appropriate models with least number of parameters. In this case, the measured ECG data may be described in terms of the parameters of the selected model. Usually, linear models are

preferred for the sake of simplicity. In the existing literature, efforts have been made to represent the ECG signals in terms of the linear combination of somewhat orthogonal functions such as complex exponentials, trigonometric functions, wavelets or pre-selected, signature functions, which best describe the signal [1-7]. For example, in [5-6], over a finite time interval, limited number of ad-hoc sinusoidal waveforms with arbitrary frequencies is selected as signature functions. Then, these forms are orthogonalized to constitute a functional base to represent the original ECG signal. Eventually, the ECG data is approximated by the weighted sum of these, so called signature base functions obtained from the previous step. In these techniques however, the optimum form of the signature base functions and the expected minimum numbers of terms in the summation, are in question. The difficulties of the above-mentioned techniques have been overcome with the novel modeling method proposed in this paper. The new method is based on the generation of the so called the "Predefined-Personalized Functional Bases or Banks - PPFB". The PPFB consist of the two major functional banks, namely the "Envelope Functions Bank - EFB" and the "Signature Functions Bank - SFB". The measured ECG data is then; modeled as the multiplication of two appropriate functions, which are retrieved within a constant from the above-mentioned banks respectively. In the following sections first the new technique to model the measured ECG data is introduced. Then, SFB, EFB and reconstruction algorithms are presented. Finally, an example is given to exhibit the utilization of the new modeling technique.

II. NEW METHOD

ECG signals are somewhat unique to a person. Moreover, on the personnel basis, it presents a quasi-stationary like behavior. Therefore, it would be appropriate to extract the statistical features of the ECG signals over a reasonable length of time. For the sake of practicality, we present the new technique on the discrete time domain since all the measurements are made with digital equipment. Let $X(n)$ be the discrete time domain representation of the measured ECG signal of a person with length N . Let this signal be analyzed frame by frame. Let $X_i(n)$ represents the portion of the original signal within frame "i". Then, we make the following "**Main Statement**" which constitutes the basis of the proposed technique in this work.

Main Statement:

(a) For any time frame "i", the measured ECG signal which is given by the vector X_i , can be expressed or approximated as

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$$X_i \equiv C_i \varphi_i \alpha_i \quad (1a)$$

where C_i is a real constant, $\varphi_i^T = [\varphi_1, \varphi_2, \varphi_3, \dots, \varphi_{L_F}]$ is a row vector. The vector $C_i \varphi_i$ carries "**almost maximum energy**" of X_i in the LMS sense. That is to say, $C_i \varphi_i$ is the best approximation of X_i with one term (i.e. $X_i \approx C_i \varphi_i$) that minimizes the sum of square error point by point, over the frame under consideration.

The $(L_F \text{ by } L_F)$ diagonal matrix $\alpha_i = \begin{bmatrix} \alpha_{i1} & 0 & \dots & 0 \\ 0 & \alpha_{i2} & & \\ 0 & & \alpha_{i3} & \\ \vdots & & & \ddots \\ 0 & & & & \alpha_{iL_F} \end{bmatrix}$ acts

as an envelope term, which may satisfy the equality or further reduce the LMS error in (1a). The integer L_F designates the total number of elements in a frame "i".

(b) In continuous time domain, (1a) takes the form of

$$X_i(t) = C_i \varphi_i(t) \alpha_i(t) \quad (1b)$$

Based on the main statement we can make the following definitions.

Definition 1a: The vector φ_i (or equivalently sequence φ_i) is called the Personalized Signature Vector (PSV) or Signature Sequence since it carries almost maximum energy of the ECG frame vector X_i with a constant C_i .

Definition 1b: In a similar manner to that of Definition 1a, the continuous time domain function $\varphi_i(t)$ is called the Personalized Signature Function (PSF).

Definition 2a: The diagonal matrix α_i (or equivalently sequence α_i) is called the Personalized Envelope Matrix (PEM) or Envelope Sequence since it matches the envelope of $C_i \varphi_i$ to the original ECG frame vector X_i .

Definition 2b: In a similar manner to that of Definition 2a, the continuous function $\alpha_i(t)$ is called the Personalized Envelope Function (PEF).

Definition 3: The real constant C_i is called the Frame Scaling Coefficient (FSC).

In order to verify the main statement, let us proceed as follows.

A discrete ECG signal $x(n)$, can be written as

$$x(n) = \sum_{i=1}^N x_i \cdot \delta_i(n-i) \quad (2a)$$

In this equation, $\delta_i(n)$ represents the unit sample; x_i designates the amplitude of the sequence $x(n)$ of length N . $x(n)$ can also be given employing the vector/matrix notation.

$$X^T = [x(1) \ x(2) \ \dots \ x(N)] = [x_1 \ x_2 \ \dots \ x_N] \quad (2b)$$

X is called the "**Main Frame vector**" and it is divided into sub-frames with equal lengths, having, for example, 8, 16 or 32 samples etc. The Frame Matrix that is represented by M_F is obtained by means of the sub-frame vectors.

$$M_F = \begin{bmatrix} X_1 & X_2 & \dots & X_{N_F} \end{bmatrix} \quad (3)$$

where

$$X_i = \begin{bmatrix} x_{(i-1)L_F+1} \\ x_{(i-1)L_F+2} \\ \vdots \\ x_{iL_F} \end{bmatrix}, \quad i = 1, 2, \dots, N_F \quad (4)$$

$N_F = N/L_F$ designates the total number of frames in X . It can be shown that each frame sequence or vector X_i can be spanned to a vector space formed by the orthonormal vectors $\{V_{ki}; k=1, 2, 3, \dots, L_F\}$, such that

$$X_i = \sum_{k=1}^{L_F} c_k V_{ki} \quad (5)$$

$$c_k = (X_i)^T V_{ki} \quad (6)$$

V_{ki} are determined by minimizing the expected value of the

error vector $\varepsilon = X_i - \sum_{k=1}^{L_F} c_k V_{ki}$ with respect to V_{ki} . This

process is called the "**determination of V_{ki} in the LMS sense**". Eventually V_{ki} are computed as the Eigenvectors of the Autocorrelation Matrix R_i of the sub-frame sequence X_i . It is straightforward to obtain the autocorrelation matrix R_i as

$$R_i = \begin{bmatrix} r_i(1) & r_i(2) & r_i(3) & \dots & r_i(L_F) \\ r_i(2) & r_i(1) & r_i(2) & \dots & r_i(L_F-1) \\ r_i(3) & r_i(2) & r_i(1) & \dots & r_i(L_F-2) \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ r_i(L_F) & r_i(L_F-1) & r_i(L_F-2) & \dots & r_i(1) \end{bmatrix} \quad (7)$$

where

$$r_i(d+1) = \frac{1}{L_F - d} \sum_{j=[(i-1)L_F+1]}^{[(iL_F)-1-d]} x_{j+1} x_{j+1+d}, \quad d=0, 1, 2, \dots, L_F-1 \quad (8)$$

It should be noted that R_i is a positive-semi definite, real symmetrical and toeplitz matrix. The above-mentioned LMS process results in the following eigen-value problem.

$$R_i V_{ki} = \lambda_{ki} V_{ki} \quad ; \quad k = 1, 2, \dots, L_F \quad (9)$$

Obviously, λ_{ki} and V_{ki} are the eigen-values and the eigenvectors of the problem under consideration. It is well known that the eigen-values of the R_i are also real and non-negative. Moreover, the eigenvectors V_{ki} are all orthonormal. Hence, (5-6) follows.

Let eigen-values be sorted in descending order such that $(\lambda_{1i} \geq \lambda_{2i} \geq \lambda_{3i} \dots \geq \lambda_{L_F i})$ with corresponding eigenvectors.

Total energy of the sub-frame "i" is given by $X_i^T X_i$

$$X_i^T X_i = \sum_{k=1}^{L_F} x_{ki}^2 = \sum_{k=1}^{L_F} c_{ki}^2 = \sum_{k=1}^{L_F} \lambda_{ki} \quad (10)$$

The eigenvectors that have the highest energy associated with the highest value of the eigen-values represent the directions of greatest variations of the signal and they are also called the principle components. Therefore, (5) may be truncated by taking the first "p" principal components, which have the highest energy of the original signal such that

$$X_i \approx \sum_{k=1}^p c_k V_{ki} \quad (11)$$

The simplest form of (10) can be obtained by setting $p=1$. The eigenvector V_{li} is called "**the major signature vector**". That is to say, the major signature vector, which has the highest energy in the LMS sense, may approximate each frame that belongs to the original ECG signal. Thus,

$$X_i \cong c_i V_{li} \quad (12)$$

In this case, the sub-frame length L_F must be selected in such a way that practically almost maximum energy is captured within the first term of (5) and the rest are negligible. Hence, (12) follows. In (12) V_{li} is also called the signature sequence since it contains most of the useful information of the original signal within the sub-frame.

Once the approximation (12) is obtained, it can be converted to equality by means of an "envelope diagonal matrix A_i " for each sub-frame. Thus, X_i is computed as

$$X_i = C_i V_{li} A_i \quad (13)$$

In (13), diagonal components a_{ir} of the Matrix A_i is computed in terms of the components v_{lir} of the Major Signature vector V_{li} and the components x_{ir} of the sub-frame vector X_i by simple division (i.e. $a_{ir} = x_{ir} / C_i v_{lir}$; $r=1,2,\dots,L_F$).

In this research work, for a person, many ECG signals were examined and thousands of sub-frames were analyzed. It has been observed that

Patterns obtained by plotting $a_i(n)=(a_{ir}$ vs. *sub-frame index*- $n=1,2,\dots,L_F$) and $v_i(n)=(v_{lir}$ vs. *sub-frame index*- $n=1,2,\dots,L_F$) exhibits repetitive similarities. Above-mentioned patterns somewhat unique to a person. Therefore, we say that ECG signals are unique to a person and exhibits quasi-stationary like behavior. It is deduced that similar patterns can be eliminated; and we can create two types of bases or banks; namely, "**envelope**" and "**signature**" banks respectively with reduced envelope and signature sequences.

Eventually, for any given sub-frame "i", the frame sequence X_i can be approximated by pulling an appropriate signature vector from the signature bank with a constant c_i , in the LMS sense (i.e. $X_i \cong c_i V_{li}$). Reduced signature vectors are renamed under the signature bank as $\{\phi_{n_s}(n); n_s=1,2,\dots,N_S\}$.

The integer N_S designates the total number of "**Signature Forms**" in the "**Signature Bank**". Similarly, reduced envelope sequences or diagonal matrices are renamed in the envelope bank as $\{\alpha_{n_e}(n); n_e=1,2,\dots,N_E\}$. The integer N_E designates the total number of "**Envelope Forms**" in the "**Envelope Bank**".

Signature and envelope sequences may as well be considered as continuous time domain functions, namely signature functions $\{\phi_{n_s}(t); n_s=1,2,\dots,N_S\}$ and envelope functions $\{\alpha_{n_e}(t); n_e=1,2,\dots,N_E\}$. These continuous functions are simply obtained by passing the corresponding sequences through a low-pass filter.

Finally, all the above explanations suggest the phrase of the main statement. Thus, we say that "any ECG signal frame X_i may be represented in terms of the multiplication of personalized envelope $\alpha_i(t)$ and signature $\phi_i(t)$ functions with a constant C_i " or $X_i(t) \cong C_i \phi_i(t) \alpha_i(t)$

In the following section, the new ECG modeling algorithms, which utilize predefined personalized envelope and signature banks is presented.

III. ALGORITHMS

The new modeling method is implemented within two major algorithmic steps. First the predefined personalized envelope and signature banks (PPFB) are generated (Algorithm 1). Then, any ECG signal is reconstructed utilizing the (PPFB) (Algorithm 2). Therefore, in this section, first Algorithm 1 is introduced. Then Algorithm 2 is outlined.

Algorithm 1: Generation of the PPFB

Inputs:

- Main Frame sequence of the ECG Signal
- Total Number of samples in the sub-frames: (L_F)

Step 1: Compute the total number of frames $N_F=N/L_F$

Step 2: Sort the Main frame X into sub-frames X_i .

Step 3: For each sub-frame X_i compute the R_i

Step 4: For each R_i compute the eigen-values λ_{ki} and the corresponding eigenvectors V_{ki} .

Step 5a: Store the eigenvector V_{ri} which is associated with the maximum eigen-value $\lambda_{ri}=\max \{ \lambda_{1i}, \lambda_{2i}, \lambda_{3i}, \dots, \lambda_{L_F i} \}$ and simply

refer this vector with the frame index, such as V_{li} .

Step 5b: Find the Frame Scaling Coefficient C_i in the LMS sense to approximate $X_i \cong C_i V_{li}$.

Step 6: Do step 5 for all the sub-frames ($i=1,2,\dots,N_F$). At the end of this step, you will be collecting the eigenvectors, which have the maximum energy for each frame.

Step 7: Compare all the collected eigenvectors in Step 6, with an efficient algorithm, and eliminate the similar ones. Thus, generate the Signature Bank $\{\phi_{n_s}(n); n_s=1,2,\dots,N_S\}$ with

reduced number of eigenvectors V_{li} . Here, N_S designates the total number of original signature patterns after the reduction.

Step 8: Compute the Diagonal Envelope Matrix A_i =diagonal $[a_{i1}, a_{i2}, \dots, a_{iL_F}]$ for each $C_i V_{li}$ computed in step 5b such that

$$a_{ir} = x_{ir} / C_i v_{lir}; r=1,2,\dots,L_F.$$

Step 9: As in Step 7, eliminate the similar patterns of envelope sequences with an efficient algorithm and create the envelope bank with reduced number original sequences $\{\alpha_{n_e}(n); n_e=1,2,\dots,N_E\}$; Here, N_E denotes the total number of original envelope patterns in the envelope bank.

The above algorithm is utilized for many different ECG signals for a person to enhance the formation of the personalized signature and envelope banks.

Once the personalized signature and envelope banks are generated, then, any ECG signal can be modeled by means of PPFB as described in Algorithm 2.

Algorithm 2: Reconstruction of ECG Signals in terms of PPFB

Inputs:

- ECG signal $\{X(n), n=1,2,\dots,N\}$ to be modeled.
- PPFB created utilizing the algorithm 1.
- L_F : Number of Samples in each sub-frame.

Step 1: Sort the sub-frames X_i as in algorithm 1.

Step 2:

(a) For each sub-frame "i" pull an appropriate signature sequence ϕ_k such that the distance or the total error

$$\delta = \|X_i - C_k \phi_k\|^2 \text{ is minimum for all } k=1,2,\dots,N_S.$$

(b) Store the index number K that refers to ϕ_K . Hence, $X_i \approx C_K \phi_K$

Step 3:

(a) Pull the appropriate envelope sequence (or diagonal matrix) α_r such that the error is further minimized for all $r=1,2,\dots,N_E$. $\delta_r = \min\{\|X_i - C_K \phi_K \alpha_r\|^2\}; r=1,2,\dots,N_E$.

(b) Store the index number R that refers to α_R .

It should be noted that at the end of this step, the best envelope α_R and signature ϕ_K patterns are found by appropriate selections. Hence, the sub-frame X_i is best described in terms of the patterns of α_R and ϕ_K . i.e. $X_i \approx \phi_K \alpha_R$.

Step 4: Having fixed α_R and ϕ_K , compute the new frame coefficient C_i to find the global minimum of the error

$\delta_{Global} = \min\{\|X_i - C_i \phi_K \alpha_R\|^2\}$ and store it. At this step, the frame sequence is approximated as $X_i \approx C_i \phi_K \alpha_R$

Step 5: Repeat the above steps for each frame to reconstruct the original ECG sequence $X(n)$.

Eventually, the above algorithm yields the frame coefficient C_i and the index numbers R and K for the best envelope and the signature sequences respectively for each frame. Thus, each frame X_i is referred by means of the FSC- C_i and the indices R and K with an acceptable error

$$\delta_{Global} = \|X_i - C_i \phi_K \alpha_R\|^2.$$

Hence, in the reproduction of ECG signals, substantial compression is achieved. Once the PPFB are stored in each communication node, then considerable amount of saving in the transmission band will be obtained.

Now, let us see the merits of the newly proposed ECG modeling technique with an example.

IV. EXAMPLE

In this example, first, several ECG signal data is recorded for a person. Each recording sampled with 500 Hz and contains 2048 samples. Then, employing the algorithm 1, we generated envelope and signature sequences bank. In the computations, the sub-frame length $N_F=16$ was selected. It was found that with an error $\delta_{Global} < 10^{-3}$, we were able to reconstruct all the measured ECG signals with 5 original signature (i.e. $N_S=5$) and 315 envelope (i.e. $N_E=315$) patterns. Let us presume that 12 bits represent each sample of the sub-frame X_i . Then, each frame of 16 samples will be represented with $12 \times 16 = 192$ bit. On the other hand, employing the newly proposed technique, each frame is described by means of C_i (FSC) and two frame indices R and K . In this example, C_i is represented by 12 bits. R and K are represented by total of 12 bits; then, 24 bits will be good enough to represent each frame. Thus, compression rate of $192/24 \approx 8$ is obtained. In

Figure 1, original and reconstructed signals are shown. As can be seen from Figure 1 that original and reconstructed signal agrees within an error of 10^{-3} .

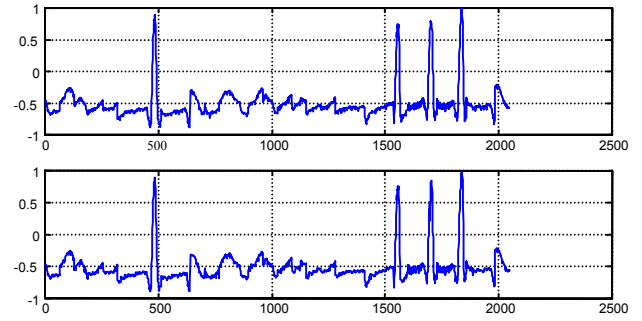


Fig. 1. Original and Reconstructed ECG Signals

V. CONCLUSION

In this paper, a novel method to represent ECG signals is presented. The proposed technique is based on the generation of the so-called, predefined personalized signature and envelope banks. It has been exhibited that the new method of modeling ECG signals, yields substantial compression and results in band saving in transmission. It is expected that detail characterization and classification of PPFB by disorders will lead to diagnosis of heart diseases in the follow-up research work.

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